

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Young, Richard S.
- (ii) TITLE OF INVENTION: Stress Proteins and Uses Therefor
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
  - (B) STREET: 2 Militia Drive
  - (C) CITY: Lexington
  - (D) STATE: MA
  - (E) COUNTRY: USA
  - (F) ZIP: 02173
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 03-NOV-1994
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: PCT/US94/06362
  - (B) FILING DATE: 06-JUN-1993
  - (C) CLASSIFICATION:
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 08/073,381
  - (B) FILING DATE: 04-JUN-1993
  - (C) CLASSIFICATION:

(ix) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/804,632
- (B) FILING DATE: 09-DEC-1991

(x) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/366,581
- (B) FILING DATE: 15-JUN-1989

(xi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/207,298
- (B) FILING DATE: 15-JUN-1988

(xii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US89/02619
- (B) FILING DATE: 15-JUN-1989

(xiii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Granahan, Patricia
- (B) REGISTRATION NUMBER: 32,227
- (C) REFERENCE/DOCKET NUMBER: WHI88-08AFA3

(xiii) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617) 861-6240

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 573 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Leu Arg Leu Pro Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg  
1                      5                      10                      15

Val	Leu	Ala	Pro	His	Leu	Thr	Arg	Ala	Tyr	Ala	Lys	Asp	Val	Lys	Phe	
			20						25					30		
Gly	Ala	Asp	Ala	Arg	Ala	Leu	Met	Leu	Gln	Gly	Val	Asp	Leu	Leu	Ala	
		35					40					45				
Asp	Ala	Val	Ala	Val	Thr	Met	Gly	Pro	Lys	Gly	Arg	Thr	Val	Ile	Ile	
	50					55					60					
Glu	Gln	Ser	Trp	Gly	Ser	Pro	Lys	Val	Thr	Lys	Asp	Gly	Val	Thr	Val	
65					70					75					80	
Ala	Lys	Ser	Ile	Asp	Leu	Lys	Asp	Lys	Tyr	Lys	Asn	Ile	Gly	Ala	Lys	
				85					90					95		
Leu	Val	Gln	Asp	Val	Ala	Asn	Asn	Thr	Asn	Glu	Glu	Ala	Gly	Asp	Gly	
			100					105					110			
Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	Arg	Ser	Ile	Ala	Lys	Glu	Gly	Phe	
		115					120					125				
Glu	Lys	Ile	Ser	Lys	Gly	Ala	Asn	Pro	Val	Glu	Ile	Arg	Arg	Gly	Val	
	130					135					140					
Met	Leu	Ala	Val	Asp	Ala	Val	Ile	Ala	Glu	Leu	Lys	Lys	Gln	Ser	Lys	
145					150					155					160	
Pro	Val	Thr	Thr	Pro	Glu	Glu	Ile	Ala	Gln	Val	Ala	Thr	Ile	Ser	Ala	
				165					170					175		
Asn	Gly	Asp	Lys	Glu	Ile	Gly	Asn	Ile	Ile	Ser	Asp	Ala	Met	Lys	Lys	
			180					185					190			
Val	Gly	Arg	Lys	Gly	Val	Ile	Thr	Val	Lys	Asp	Gly	Lys	Thr	Leu	Asn	
		195					200					205				
Asp	Glu	Leu	Glu	Ile	Ile	Glu	Gly	Met	Lys	Phe	Asp	Arg	Gly	Tyr	Ile	
	210					215					220					

Ser	Pro	Tyr	Phe	Ile	Asn	Thr	Ser	Lys	Gly	Gln	Lys	Cys	Glu	Phe	Gln
225					230					235					240
Asp	Ala	Tyr	Val	Leu	Leu	Ser	Glu	Lys	Lys	Ile	Ser	Ser	Ile	Gln	Ser
			245						250					255	
Ile	Val	Pro	Ala	Leu	Glu	Ile	Ala	Asn	Ala	His	Arg	Lys	Pro	Leu	Val
			260					265						270	
Ile	Ile	Ala	Glu	Asp	Val	Asp	Gly	Glu	Ala	Leu	Ser	Thr	Leu	Val	Leu
		275					280					285			
Asn	Arg	Leu	Lys	Val	Gly	Leu	Gln	Val	Val	Ala	Val	Lys	Ala	Pro	Gly
		290				295						300			
Phe	Gly	Asp	Asn	Arg	Lys	Asn	Gln	Leu	Lys	Asp	Met	Ala	Ile	Ala	Thr
305					310					315					320
Gly	Gly	Ala	Val	Phe	Gly	Glu	Glu	Gly	Leu	Thr	Leu	Asn	Leu	Glu	Asp
				325					330					335	
Val	Gln	Pro	His	Asp	Leu	Gly	Lys	Val	Gly	Glu	Val	Ile	Val	Thr	Lys
			340					345						350	
Asp	Asp	Ala	Met	Leu	Leu	Lys	Gly	Lys	Gly	Asp	Lys	Ala	Gln	Ile	Glu
		355					360					365			
Lys	Arg	Ile	Gln	Glu	Ile	Ile	Glu	Gln	Leu	Asp	Val	Thr	Thr	Ser	Glu
		370				375						380			
Tyr	Glu	Lys	Glu	Lys	Leu	Asn	Glu	Arg	Leu	Ala	Lys	Leu	Ser	Asp	Gly
385					390					395					400
Val	Ala	Val	Leu	Lys	Val	Gly	Gly	Thr	Ser	Asp	Val	Glu	Val	Asn	Glu
				405					410					415	
Lys	Lys	Asp	Arg	Val	Thr	Asp	Ala	Leu	Asn	Ala	Thr	Arg	Ala	Ala	Val
			420					425					430		
Glu	Glu	Gly	Ile	Val	Leu	Gly	Gly	Gly	Cys	Ala	Leu	Leu	Arg	Cys	Ile
		435					440					445			

Pro Ala Leu Asp Ser Leu Thr Pro Ala Asn Glu Asp Gln Lys Ile Gly  
450 455 460

Ile Glu Ile Ile Lys Arg Thr Leu Lys Ile Pro Ala Met Thr Ile Ala  
465 470 475 480

Lys Asn Ala Gly Val Glu Gly Ser Leu Ile Val Glu Lys Ile Met Gln  
485 490 495

Ser Ser Ser Glu Val Gly Tyr Asp Ala Met Ala Gly Asp Phe Val Asn  
500 505 510

Met Val Glu Lys Gly Ile Ile Asp Pro Thr Lys Val Val Arg Thr Ala  
515 520 525

Leu Leu Asp Ala Ala Gly Val Ala Ser Leu Leu Thr Thr Ala Glu Val  
530 535 540

Val Val Thr Glu Ile Pro Lys Glu Glu Lys Asp Pro Gly Met Gly Ala  
545 550 555 560

Met Gly Gly Met Gly Gly Gly Met Gly Gly Gly Met Phe  
565 570

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met  
1 5 10 15

Leu	Arg	Gly	Val	Asn	Val	Leu	Ala	Asp	Ala	Val	Lys	Val	Thr	Leu	Gly	20	25	30	
Pro	Lys	Gly	Arg	Asn	Val	Val	Leu	Asp	Lys	Ser	Phe	Gly	Ala	Pro	Thr	35	40	45	
Ile	Thr	Lys	Asp	Gly	Val	Ser	Val	Ala	Arg	Glu	Ile	Glu	Pro	Glu	Asp	50	55	60	
Lys	Phe	Glu	Asn	Met	Gly	Ala	Gln	Met	Val	Lys	Glu	Val	Ala	Ser	Lys	65	70	75	80
Ala	Asn	Asp	Ala	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala	Thr	Val	Leu	Ala	85	90	95	
Gln	Ala	Ile	Ile	Thr	Glu	Gly	Leu	Lys	Ala	Val	Ala	Ala	Gly	Met	Asn	100	105	110	
Pro	Met	Asp	Leu	Lys	Arg	Gly	Ile	Asp	Lys	Ala	Val	Thr	Ala	Ala	Val	115	120	125	
Glu	Glu	Leu	Lys	Ala	Leu	Ser	Val	Pro	Cys	Ser	Asp	Ser	Lys	Ala	Ile	130	135	140	
Ala	Gln	Val	Gly	Thr	Ile	Ser	Ala	Asn	Ser	Asp	Glu	Thr	Val	Gly	Lys	145	150	155	160
Leu	Ile	Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Lys	Glu	Gly	Val	Ile	Thr	165	170	175	
Val	Glu	Asp	Gly	Thr	Gly	Leu	Gln	Asp	Glu	Leu	Asp	Val	Val	Glu	Gly	180	185	190	
Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	Ile	Asn	Lys	Pro	195	200	205	
Glu	Thr	Gly	Ala	Val	Glu	Leu	Glu	Ser	Pro	Phe	Ile	Leu	Leu	Ala	Asp	210	215	220	

Lys	Lys	Ile	Ser	Asn	Ile	Arg	Glu	Met	Leu	Pro	Val	Leu	Glu	Ala	Val	225	230	235	240
Ala	Lys	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	Asp	Val	Glu	Gly	245	250	255	
Glu	Ala	Leu	Ala	Thr	Ala	Val	Val	Asn	Thr	Ile	Arg	Gly	Ile	Val	Lys	260	265	270	
Val	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	Arg	Lys	Ala	Met	275	280	285	
Leu	Gln	Asp	Ile	Ala	Thr	Leu	Thr	Gly	Gly	Thr	Val	Ile	Ser	Glu	Glu	290	295	300	
Ile	Gly	Met	Glu	Leu	Glu	Lys	Ala	Thr	Leu	Glu	Asp	Leu	Gly	Gln	Ala	305	310	315	320
Lys	Arg	Val	Val	Ile	Asn	Lys	Asp	Thr	Thr	Thr	Ile	Ile	Asp	Gly	Val	325	330	335	
Gly	Glu	Glu	Ala	Ala	Ile	Gln	Gly	Arg	Val	Ala	Gln	Ile	Arg	Gln	Gln	340	345	350	
Ile	Glu	Glu	Ala	Thr	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	Leu	Gln	Glu	Arg	355	360	365	
Val	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	Val	Gly	Ala	Ala	370	375	380	
Thr	Glu	Val	Glu	Met	Lys	Glu	Lys	Lys	Ala	Arg	Val	Glu	Asp	Ala	Leu	385	390	395	400
His	Ala	Thr	Arg	Ala	Ala	Val	Glu	Glu	Gly	Val	Val	Ala	Gly	Gly	Gly	405	410	415	
Val	Ala	Leu	Ile	Arg	Val	Ala	Ser	Lys	Leu	Ala	Asp	Leu	Arg	Gly	Gln	420	425	430	
Asn	Glu	Asp	Gln	Asn	Val	Val	Ser	Ser	Ser	Leu	Arg	Ala	Met	Glu	Ala	435	440	445	

Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu Glu Pro Ser Val Val  
450 455 460

Ala Asn Thr Val Lys Gly Gly Asp Gly Asn Tyr Gly Tyr Asn Ala Ala  
465 470 475 480

Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly Ile Leu Asp Pro Thr  
485 490 495

Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala Ser Val Ala Gly Leu  
500 505 510

Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu Pro Lys Asn Asp Ala  
515 520 525

Ala Asp Leu Gly Ala Ala Gly Gly Met Gly Gly Met Gly Gly Met Gly  
530 535 540

Gly Met Met  
545

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu  
1 5 10 15

Arg Gly Leu Asn Ser Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro  
20 25 30

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Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile  
 35 40 45  
 Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro  
 50 55 60  
 Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr  
 65 70 75 80  
 Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln  
 85 90 95  
 Ala Leu Val Lys Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro  
 100 105 110  
 Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Asp Lys Val Thr Glu  
 115 120 125  
 Thr Leu Leu Lys Asp Ala Lys Glu Val Glu Thr Lys Glu Gln Ile Ala  
 130 135 140  
 Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile  
 145 150 155 160  
 Ala Glu Ala Met Asp Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu  
 165 170 175  
 Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg  
 180 185 190  
 Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Ala Glu Arg  
 195 200 205  
 Gln Glu Ala Val Leu Glu Glu Pro Tyr Ile Leu Leu Val Ser Ser Lys  
 210 215 220  
 Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gln  
 225 230 235 240

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Ala Gly Lys Ser Leu Leu Ile Ile	Ala Glu Asp Val Glu Gly Glu Ala
245	255
Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val	
260	270
Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln	
275	285
Asp Met Ala Ile Leu Thr Gly Ala Gln Val Ile Ser Glu Glu Val Gly	
290	300
Leu Thr Leu Glu Asn Thr Asp Leu Ser Leu Leu Gly Lys Ala Arg Lys	
305	320
Val Val Met Thr Lys Asp Glu Thr Thr Ile Val Glu Gly Ala Gly Asp	
325	335
Thr Asp Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Thr Glu Ile Glu	
340	350
Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala	
355	365
Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu	
370	380
Val Glu Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asn	
385	400
Ala Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Val Thr	
405	415
Leu Leu Gln Ala Ala Pro Ala Leu Asp Lys Leu Lys Leu Thr Gly Asp	
420	430
Glu Ala Thr Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu	
435	445
Lys Gln Ile Ala Phe Asn Ser Gly Met Glu Pro Gly Val Val Ala Glu	
450	460

Lys Val Arg Asn Leu Ser Val Gly His Gly Leu Asn Ala Ala Thr Gly  
465 470 475 480

Glu Tyr Glu Asp Leu Leu Lys Ala Gly Val Ala Asp Pro Val Lys Val  
485 490 495

Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu Phe Thr  
500 505 510

Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Thr Ala Ala Pro Ala  
515 520 525

Ser Asp Pro Thr Gly Gly Met Gly Gly Met Asp Phe  
530 535 540

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Lys Thr Ile Ala Tyr Asp Glu Glu Ala Arg Arg Gly Leu Glu  
1 5 10 15

Arg Gly Leu Asn Ala Leu Ala Asp Ala Val Lys Val Thr Leu Gly Pro  
20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Lys Trp Gly Ala Pro Thr Ile  
35 40 45

Thr Asn Asp Gly Val Ser Ile Ala Lys Glu Ile Glu Leu Glu Asp Pro  
50 55 60

Tyr Glu Lys Ile Gly Ala Glu Leu Val Lys Glu Val Ala Lys Lys Thr  
65 70 75 80

Asp Asp Val Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Gln  
85 90 95

Ala Leu Arg Lys Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro  
100 105 110

Leu Gly Leu Lys Arg Gly Ile Glu Lys Ala Val Glu Lys Val Thr Glu  
115 120 125

Thr Leu Leu Lys Gly Ala Lys Glu Val Glu Thr Lys Glu Gln Ile Ala  
130 135 140

Ala Thr Ala Ala Ile Ser Ala Gly Asp Gln Ser Ile Gly Asp Leu Ile  
145 150 155 160

Ala Glu Ala Met Asp Lys Val Gly Asn Glu Gly Val Ile Thr Val Glu  
165 170 175

Glu Ser Asn Thr Phe Gly Leu Gln Leu Glu Leu Thr Glu Gly Met Arg  
180 185 190

Phe Asp Lys Gly Tyr Ile Ser Gly Tyr Phe Val Thr Asp Pro Glu Arg  
195 200 205

Gln Glu Ala Val Leu Glu Asp Pro Tyr Ile Leu Leu Val Ser Ser Lys  
210 215 220

Val Ser Thr Val Lys Asp Leu Leu Pro Leu Leu Glu Lys Val Ile Gly  
225 230 235 240

Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Ala  
245 250 255

Leu Ser Thr Leu Val Val Asn Lys Ile Arg Gly Thr Phe Lys Ser Val  
260 265 270

Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Gln  
275 280 285

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Asp Met Ala Ile Leu Thr Gly Gly Gln Val Ile Ser Glu Glu Val Gly  
290 295 300

Leu Thr Leu Glu Asn Ala Asp Leu Ser Leu Leu Gly Lys Ala Arg Lys  
305 310 315 320

Val Val Val Thr Lys Asp Glu Thr Thr Ile Val Glu Gly Ala Gly Asp  
325 330 335

Thr Asp Ala Ile Ala Gly Arg Val Ala Gln Ile Arg Gln Glu Ile Glu  
340 345 350

Asn Ser Asp Ser Asp Tyr Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala  
355 360 365

Lys Leu Ala Gly Gly Val Ala Val Ile Lys Ala Gly Ala Ala Thr Glu  
370 375 380

Val Glu Leu Lys Glu Arg Lys His Arg Ile Glu Asp Ala Val Arg Asn  
385 390 395 400

Ala Lys Ala Ala Val Glu Glu Gly Ile Val Ala Gly Gly Gly Val Thr  
405 410 415

Leu Leu Gln Ala Ala Pro Thr Leu Asp Glu Leu Lys Leu Glu Gly Asp  
420 425 430

Glu Ala Thr Gly Ala Asn Ile Val Lys Val Ala Leu Glu Ala Pro Leu  
435 440 445

Lys Gln Ile Ala Phe Asn Ser Gly Leu Glu Pro Gly Val Val Ala Glu  
450 455 460

Lys Val Arg Asn Leu Pro Ala Gly His Gly Leu Asn Ala Gln Thr Gly  
465 470 475 480

Val Tyr Glu Asp Leu Leu Ala Ala Gly Val Ala Asp Pro Val Lys Val  
485 490 495

Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Ile Ala Gly Leu Phe Leu  
500 505 510

Thr Thr Glu Ala Val Val Ala Asp Lys Pro Glu Lys Glu Lys Ala Ser  
515 520 525

Val Pro Gly Gly Gly Asp Met Gly Gly Met Asp Phe  
530 535 540